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Range: from to Features: ☐ SNP ☒ CDD ☒ MGC ☒ HPRD ☒ STS ☒ tRNA

BLink, Conserved
Domains, Links☐ 1: P08887. Reports Interleukin-6 rec...[gi:124343]Comment Features Sequence

LOCUS P08887 468 aa linear PRI 07-FEB-2006
DEFINITION Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R
1) (Membrane glycoprotein 80) (gp80) (CD126 antigen).
ACCESSION P08887
VERSION P08887 GI:124343
DBSOURCE swissprot: locus IL6RA_HUMAN, accession P08887;
class: standard.
extra accessions: Q16202, Q53EQ7, Q5FWG2, Q5VZ23, created: Nov 1, 1988.
sequence updated: Nov 1, 1988.
annotation updated: Feb 7, 2006.
xrefs: X12830.1, CAA31312.1, X58298.1, CAA41231.1, AK223582.1,
BAD97302.1, AL162591.16, CAH72853.1, BC089410.1, AAH89410.1,
S72848.1, AAC60635.1, A41242, 1N26A, 1N2Q_C, 1N2Q_D, 1P9MC
xrefs (non-sequence databases): IntAct:P08887,
Ensembl:ENSG00000160712, HGNC:6019, MIM: 147880, LinkHub:P08887,
GO:0005576, GO:0005896, GO:0019899, GO:0004915, GO:0008283,
GO:0007166, GO:0007275, GO:0006955, InterPro:IPR002996,
InterPro:IPR003961, InterPro:IPR003530, InterPro:IPR003599,
InterPro:IPR007110, InterPro:IPR003598, Pfam:PF00041, Pfam:PF00047,
SMART:SM00060, SMART:SM00409, SMART:SM00408, PROSITE:PS50853,
PROSITE:PS01354, PROSITE:PS50835
KEYWORDS 3D-structure; Alternative splicing; Direct protein sequencing;
Glycoprotein; Immunoglobulin domain; Membrane; Polymorphism;
Receptor; Signal; Transmembrane.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (residues 1 to 468)
AUTHORS Yamasaki,K., Taga,T., Hirata,Y., Yawata,H., Kawanishi,Y., Seed,B.,
Taniguchi,T., Hirano,T. and Kishimoto,T.
TITLE Cloning and expression of the human interleukin-6 (BSF-2/IFN beta
2) receptor
JOURNAL Science 241 (4867), 825-828 (1988)
PUBMED 3136546
REMARK NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
REFERENCE 2 (residues 1 to 468)
AUTHORS Yamasaki,K., Taga,T., Hirata,Y., Yawata,H., Kawanishi,Y., Seed,B.,
Taniguchi,T., Hirano,T. and Kishimoto,T.
TITLE Molecular structure of interleukin 6 receptor
JOURNAL Proc. Jpn. Acad., B, Phys. Biol. Sci. 64, 209-211 (1988)
REMARK NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
REFERENCE 3 (residues 1 to 468)
AUTHORS Schooltink,H., Stoyan,T., Lenz,D., Schmitz,H., Hirano,T.,
Kishimoto,T., Heinrich,P.C. and Rose-John,S.
TITLE Structural and functional studies on the human hepatic
interleukin-6 receptor. Molecular cloning and overexpression in
HepG2 cells
JOURNAL Biochem. J. 277 (PT 3), 659-664 (1991)
PUBMED 1872801
REMARK NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
REFERENCE 4 (residues 1 to 468)
AUTHORS Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A. and
Yokoyama,S.
TITLE Direct Submission
JOURNAL Submitted (??-APR-2005)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
TISSUE=Kidney

REFERENCE 5 (residues 1 to 468)
AUTHORS
CONSRM Human chromosome 1 international sequencing consortium
TITLE Direct Submission
JOURNAL Submitted (??-MAY-2005)
REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

REFERENCE 6 (residues 1 to 468)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
TISSUE=Lymph

REFERENCE 7 (residues 1 to 468)
AUTHORS Horiuchi,S., Koyanagi,Y., Zhou,Y., Miyamoto,H., Tanaka,Y., Waki,M., Matsumoto,A., Yamamoto,M. and Yamamoto,N.
TITLE Soluble interleukin-6 receptors released from T cell or granulocyte/macrophage cell lines and human peripheral blood mononuclear cells are generated through an alternative splicing mechanism
JOURNAL Eur. J. Immunol. 24 (8), 1945-1948 (1994)
PUBMED 8056053
REMARK NUCLEOTIDE SEQUENCE [MRNA] OF 313-365 (ISOFORM 2).

REFERENCE 8 (residues 1 to 468)
AUTHORS Cole,A.R., Hall,N.E., Treutlein,H.R., Eddes,J.S., Reid,G.E., Moritz,R.L. and Simpson,R.J.
TITLE Disulfide bond structure and N-glycosylation sites of the extracellular domain of the human interleukin-6 receptor
JOURNAL J. Biol. Chem. 274 (11), 7207-7215 (1999)
PUBMED 10066782
REMARK PARTIAL PROTEIN SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.

REFERENCE 9 (residues 1 to 468)
AUTHORS Novick,D., Engelmann,H., Wallach,D. and Rubinstein,M.
TITLE Soluble cytokine receptors are present in normal human urine
JOURNAL J. Exp. Med. 170 (4), 1409-1414 (1989)
PUBMED 2529343
REMARK PROTEIN SEQUENCE OF 20-49, AND SUBCELLULAR LOCATION.

REFERENCE 10 (residues 1 to 468)
AUTHORS Yawata,H., Yasukawa,K., Natsuka,S., Murakami,M., Yamasaki,K., Hibi,M., Taga,T. and Kishimoto,T.
TITLE Structure-function analysis of human IL-6 receptor: dissociation of amino acid residues required for IL-6-binding and for IL-6 signal transduction through gp130
JOURNAL EMBO J. 12 (4), 1705-1712 (1993)
PUBMED 8467812
REMARK MUTAGENESIS.

REFERENCE 11 (residues 1 to 468)
AUTHORS Martens,A.S., Bode,J.G., Heinrich,P.C. and Graeve,L.
TITLE The cytoplasmic domain of the interleukin-6 receptor gp80 mediates its basolateral sorting in polarized madin-darby canine kidney cells
JOURNAL J. Cell. Sci. 113 (PT 20), 3593-3602 (2000)
PUBMED 11017875
REMARK FUNCTION.

REFERENCE 12 (residues 1 to 468)

AUTHORS Buk,D.M., Renner,O. and Graeve,L.
 TITLE Increased association with detergent-resistant membranes/lipid rafts of apically targeted mutants of the interleukin-6 receptor gp80
 JOURNAL Eur. J. Cell Biol. 84 (10), 819-831 (2005)
 PUBMED 16270750
 REMARK FUNCTION, AND SUBCELLULAR LOCATION.
 REFERENCE 13 (residues 1 to 468)
 AUTHORS Varghese,J.N., Moritz,R.L., Lou,M.Z., Van Donkelaar,A., Ji,H., Ivancic,N., Branson,K.M., Hall,N.E. and Simpson,R.J.
 TITLE Structure of the extracellular domains of the human interleukin-6 receptor alpha -chain
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (25), 15959-15964 (2002)
 PUBMED 12461182
 REMARK X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 20-344.
 COMMENT On or before Dec 27, 2005 this sequence version replaced gi:74754774, gi:74755342, gi:74757093, gi:106829.
 [FUNCTION] Part of the receptor for interleukin 6. Binds to IL-6 with low affinity, but does not transduce a signal. Signal activation necessitate an association with IL6ST. Activation may lead to the regulation of the immune response, acute-phase reactions and hematopoiesis.
 [FUNCTION] Low concentration of a soluble form of interleukin-6 receptor acts as an agonist of IL6 activity.
 [SUBUNIT] Hexamer of two molecules each of IL6, IL6R and IL6ST.
 [INTERACTION] Q9NZ08:ARTS-1; NbExp=1; IntAct=EBI-299383, EBI-299412.
 [SUBCELLULAR LOCATION] Type I membrane protein (isoform 1); basolateral membrane. Secreted (isoform 2).
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; Synonyms=Long; IsoId=P08887-1; Sequence=Displayed; Name=2; Synonyms=Short; IsoId=P08887-2; Sequence=VSP_001682, VSP_001683.
 [TISSUE SPECIFICITY] Isoform 2 is expressed in peripheral blood mononuclear cells and weakly found in urine and serum.
 [DOMAIN] The two fibronectin type-III-like domains, contained in the N-terminal part, form together a cytokine-binding domain.
 [DOMAIN] The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
 [PTM] A short soluble form may also be released from the membrane by proteolysis.
 [SIMILARITY] Belongs to the type I cytokine receptor family. Type 3 subfamily.
 [SIMILARITY] Contains 1 fibronectin type-III domain.
 [SIMILARITY] Contains 1 Ig-like C2-type (immunoglobulin-like) domain.

FEATURES

source	1..468 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..468 /gene="IL6R"
Protein	1..468 /gene="IL6R" /product="Interleukin-6 receptor alpha chain precursor"
Region	1..19 /gene="IL6R" /region_name="Signal" /experiment="experimental evidence, no additional details recorded"
Region	20..468 /gene="IL6R" /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="Interleukin-6 receptor alpha chain." /FTId=PRO_0000010895."
Region	20..365 /gene="IL6R" /region_name="Topological domain" /inference="non-experimental evidence, no additional details recorded" /note="Extracellular (Potential)."
Region	22..23 /gene="IL6R" /region_name="Beta-strand region"

Bond /experiment="experimental evidence, no additional details recorded"
bond(25,193)
/gene="IL6R"
/bond_type="disulfide"
/experiment="experimental evidence, no additional details recorded"

Region 26..112
/gene="IL6R"
/region_name="Domain"
/experiment="experimental evidence, no additional details recorded"
/note="Ig-like C2-type."

Region 32..33
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 34..37
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 39..>96
/gene="IL6R"
/region_name="Immunoglobulin like"
/note="IG_like"
/db_xref="CDD:5322"

Region 39..40
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 43..46
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Bond bond(47,96)
/gene="IL6R"
/bond_type="disulfide"
/experiment="experimental evidence, no additional details recorded"

Region 48..49
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 50
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 52..53
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Site 55
/gene="IL6R"
/site_type="glycosylation"
/experiment="experimental evidence, no additional details recorded"
/note="N-linked (GlcNAc...)."

Region 56..63
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/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 65..68
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 72..83
/gene="IL6R"
/region_name="Beta-strand region"

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            /region_name="Beta-strand region"
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Region      88..90
            /gene="IL6R"
            /region_name="Helical region"
            /experiment="experimental evidence, no additional details
recorded"
Region      92..101
            /gene="IL6R"
            /region_name="Beta-strand region"
            /experiment="experimental evidence, no additional details
recorded"
Site        93
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            /site_type="glycosylation"
            /experiment="experimental evidence, no additional details
recorded"
            /note="N-linked (GlcNAc...)."
Region      103
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            /region_name="Beta-strand region"
            /experiment="experimental evidence, no additional details
recorded"
Region      105..110
            /gene="IL6R"
            /region_name="Beta-strand region"
            /experiment="experimental evidence, no additional details
recorded"
Region      120..125
            /gene="IL6R"
            /region_name="Beta-strand region"
            /experiment="experimental evidence, no additional details
recorded"
Bond        bond(121,132)
            /gene="IL6R"
            /bond_type="disulfide"
            /experiment="experimental evidence, no additional details
recorded"
Site        121
            /gene="IL6R"
            /site_type="mutagenized"
            /experiment="experimental evidence, no additional details
recorded"
            /note="C->S: Complete loss of ligand-binding."
Site        122
            /gene="IL6R"
            /site_type="mutagenized"
            /experiment="experimental evidence, no additional details
recorded"
            /note="F->A: No change of ligand-binding and IL6
signaling."
Region      126..127
            /gene="IL6R"
            /region_name="Hydrogen bonded turn"
            /experiment="experimental evidence, no additional details
recorded"
Region      128
            /gene="IL6R"
            /region_name="Beta-strand region"
            /experiment="experimental evidence, no additional details
recorded"
Region      130..134
            /gene="IL6R"
            /region_name="Beta-strand region"
            /experiment="experimental evidence, no additional details
recorded"
Site        132
            /gene="IL6R"
            /site_type="mutagenized"
            /experiment="experimental evidence, no additional details
recorded"
            /note="C->A: Complete loss of ligand-binding."

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Site 134
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="W->L: Complete loss of ligand-binding."

Region 137..138
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"

Site 140
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="P->G: No change of ligand-binding and IL6 signaling."

Region 142..143
 /gene="IL6R"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details recorded"

Region 145..157
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"

Site 153
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="F->L: No change of ligand-binding and IL6 signaling."

Region 159..168
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"

Bond bond(165,176)
 /gene="IL6R"
 /bond_type="disulfide"
 /experiment="experimental evidence, no additional details recorded"

Site 165
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="C->L: Complete loss of ligand-binding."

Region 169..172
 /gene="IL6R"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details recorded"

Region 173..178
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"

Site 174
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="F->L: No change of ligand-binding and IL6 signaling."

Site 176
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="C->A: Complete loss of ligand-binding."

Region 182..183
 /gene="IL6R"
 /region_name="Hydrogen bonded turn"

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/experiment="experimental evidence, no additional details
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Site 184
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="D->T: 30% decrease of ligand-binding and IL6
signaling."
Region 187..196
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
Site 190
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="V->G: 80% decrease of ligand-binding and no IL6
signaling."
Site 193
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="C->D: Complete loss of ligand-binding."
Region 197..198
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
recorded"
Region 199..202
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
Region 206..209
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
Region 210..212
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
recorded"
Region 210
/gene="IL6R"
/region_name="Conflict"
/experiment="experimental evidence, no additional details
recorded"
/note="G -> D (in Ref. 4)."
Site 211
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="C->A: No change of ligand-binding and IL6
signaling."
Region 214
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
Region 216..311
/gene="IL6R"
/region_name="Domain"
/experiment="experimental evidence, no additional details
recorded"
/note="Fibronectin type-III."
Region 216..308
/gene="IL6R"
/region_name="Fibronectin type 3 domain"
/note="FN3"
/db_xref="CDD:14799"
Site 217

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Region /gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="D->V: Complete loss of ligand-binding."
220..226

Site /gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
221

Region /gene="IL6R"
/site_type="glycosylation"
/experiment="experimental evidence, no additional details recorded"
/note="N-linked (GlcNAc...)."
228..229

Region /gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
231..232

Site /gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="R->S: 30% decrease of ligand-binding and IL6 signaling."
232

Site /gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="W->Q: 30% decrease of ligand-binding and increase of IL6 signaling."
233

Region /gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
234..239

Region /gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
242..243

Site /gene="IL6R"
/site_type="glycosylation"
/experiment="experimental evidence, no additional details recorded"
/note="N-linked (GlcNAc...)."
245

Region /gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
247..249

Region /gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
251..259

Site /gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="E->A: 50% decrease of ligand-binding and IL6 signaling."
254

Region /gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
260..261

Region recorded"
263
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 266..269
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 271..273
/gene="IL6R"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

Region 275..281
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 277
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="C->D: 30% increase of ligand-binding and 100% increase in IL6 signaling."

Site 278
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="V->N: 50% Decrease of ligand-binding and 50% increase in IL6 signaling."

Site 279
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/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="I->D: Complete loss of ligand-binding."

Site 280
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/experiment="experimental evidence, no additional details recorded"
/note="H->I: No change of ligand-binding and no IL6 signaling."

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/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="D->G: 70% decrease of ligand-binding and no IL6 signaling."

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Site 285
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/experiment="experimental evidence, no additional details recorded"
/note="G->D: 80% decrease of ligand-binding and no IL6 signaling."

Region 288..296
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/experiment="experimental evidence, no additional details recorded"

Site 291
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"

/note="Q->K: Complete loss of ligand-binding."
Site 293
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 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="R->G: Complete loss of ligand-binding."
Region 297..299
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 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details recorded"
Region 300..301
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"
Region 303..307
 /gene="IL6R"
 /region_name="Short sequence motif of biological interest"
 /experiment="experimental evidence, no additional details recorded"
 /note="WSXWS motif."
Region 310..312
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"
Region 356..365
 /gene="IL6R"
 /region_name="Splicing variant"
 /experiment="experimental evidence, no additional details recorded"
 /note="VQDSSSVPLP -> GSRRRGSCGL (in isoform 2).
 /FTId=VSP_001682."
Region 358
 /gene="IL6R"
 /region_name="Variant"
 /experiment="experimental evidence, no additional details recorded"
 /note="D -> A (in dbSNP:8192284). /FTId=VAR_021995."
Region 366..468
 /gene="IL6R"
 /region_name="Splicing variant"
 /experiment="experimental evidence, no additional details recorded"
 /note="Missing (in isoform 2). /FTId=VSP_001683."
Region 366..386
 /gene="IL6R"
 /region_name="Transmembrane region"
 /inference="non-experimental evidence, no additional details recorded"
 /note="Potential."
Region 387..468
 /gene="IL6R"
 /region_name="Topological domain"
 /inference="non-experimental evidence, no additional details recorded"
 /note="Cytoplasmic (Potential)."

ORIGIN

```

1  mlavgcalla  allaapgaal  aprrcpagev  argvltslpg  dsvtltcpgv  epednatvhw
61  vlrkpaagsh  psrwagmgr  lllrsvqlhd  sgnyscyrag  rpagtvhllv  dvppeepqls
121 cfrksplsnv  vcewgprstp  slttkavllv  rkfqnspace  fgepcqysqe  sqkfscqlav
181 pegdssfyiv  smcvassvgs  kfsktqtfgg  cgilqpdppa  nitvtavarn  prwlsvtwqd
241 phswnsffyr  lrfelryrae  rsktfttmv  kdlqhhcvi  dawsglrhvv  qlraqeefgq
301 gewsewspea  mgtpwtesrs  ppaenevstp  mgalttnkdd  dnlfdrsan  atslpvqdss
361 svplptflva  ggslafgtll  ciaivlrffk  twklralkeg  ktsmhppysl  gqlvperprp
421 tpvlvplisp  pvspsslgd  ntsshnrpda  rdprspydis  ntdyffpr

```

//

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Feb 1 2006 13:21:03